

(FILE 'HOME' ENTERED AT 11:09:22 ON 27 OCT 2004)

FILE 'MEDLINE, CAPLUS, BIOSIS, AGRICOLA' ENTERED AT 11:09:29 ON 27 OCT 2004

L1	7 S CUVULARIA
L2	0 S L1 AND PALLESCENS
L3	861 S PALLESCENS
L4	0 S OXIDOREDUCTASE AND L3
L5	23 S L3 AND OXI?
L6	20 DUP REM L5 (3 DUPLICATES REMOVED)

=>

Database : Issued_Patents_AA:*

- 1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
- 2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
- 3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
- 4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
- 5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
- 6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		%					
No.	Score	Query Match	Length	DB	ID	Description	
1	3336	100.0	627	4	US-09-468-578-7	Sequence 7, Appli	
2	3336	100.0	627	4	US-09-868-839-7	Sequence 7, Appli	6,509,509
3	3168	95.0	627	4	US-09-468-578-4	Sequence 4, Appli	
4	3168	95.0	627	4	US-09-868-839-4	Sequence 4, Appli	
5	1929.5	57.8	594	4	US-09-468-578-2	Sequence 2, Appli	
6	1929.5	57.8	594	4	US-09-218-702-2	Sequence 2, Appli	
7	1929.5	57.8	594	4	US-09-868-839-2	Sequence 2, Appli	
8	1795	53.8	572	3	US-09-401-476-4	Sequence 4, Appli	
9	1776	53.2	568	4	US-09-218-702-4	Sequence 4, Appli	

102(2)

Database : A_Geneseq_29Jan04:*

- 1: geneseqp1980s:*
- 2: geneseqp1990s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	3336	100.0	627	3	AAy96763	Aay96763 Curvulari
2	3336	100.0	627	3	AAy95539	Aay95539 Curvulari
3	3336	100.0	627	5	AAO18212	Aao18212 C pallesc
4	3168	95.0	627	3	AAy96762	Aay96762 Bipolaris
5	3168	95.0	627	3	AAy95538	Aay95538 Bipolaris
6	3168	95.0	627	5	AAO18211	Aao18211 B spicife
7	3168	95.0	627	6	ABG75578	Abg75578 B. spicif
8	2548	76.4	480	6	ABG75579	Abg75579 C. palles
9	1929.5	57.8	594	2	AAy45222	Aay45222 Stachybot
10	1929.5	57.8	594	2	AAy39992	Aay39992 Stachybot
11	1929.5	57.8	594	3	AAy96761	Aay96761 Stachybot
12	1929.5	57.8	594	3	AAy95537	Aay95537 Stachybot
13	1929.5	57.8	594	5	AAO18210	Aao18210 S chartar
14	1929.5	57.8	594	6	ABG75577	Abg75577 S. charta
15	1795	53.8	572	2	AAR40843	Aar40843 Bilirubin
16	1761.5	52.8	602	3	AAy69204	Aay69204 Amino aci
17	1743.5	52.3	583	5	AAU97316	Aau97316 Phenol ox
18	1743.5	52.3	583	5	ABB75770	Abb75770 Phenol ox

RESULT 2

AA95539

ID AAY95539 standard; protein; 627 AA.

XX

AC AAY95539;

XX

DT 10-OCT-2000 (first entry)

XX

DE *Curvularia pallescens* phenol oxidising enzyme.

XX

KW Phenol oxidising enzyme; detergent; bleaching.

XX

OS *Curvularia pallescens*.

XX

PN WO200039306-A2.

XX

PD 06-JUL-2000.

XX

PF 20-DEC-1999; 99WO-EP010287.

XX

PR 23-DEC-1998; 98US-00220871.

PR 23-JUN-1999; 99US-00338723.

XX

PA (UNIL) UNILEVER NV.

PA (UNIL) UNILEVER PLC.

PA (HIND-) HINDUSTAN LEVER LTD.

XX

PI Bodie EA, Van Der Velden S, De Vries CH, Wang H;

XX

DR WPI; 2000-514528/46.

DR N-PSDB; AAA50021.

XX

PT Detergent composition comprising novel phenol oxidizing enzyme obtained from fungus or bacteria, useful for pulp and paper bleaching, bleaching color of stains on fabric and for anti-dye redeposition.

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PS Claim 8; Fig 10; 45pp; English.

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CC The present sequence is that of the *Curvularia pallescens* phenol oxidising enzyme. The invention relates to detergent compositions comprising novel phenol oxidising enzymes that have at least 60% identity with the phenol oxidising enzyme of *Stachybotrys chartarum* (see AAY95537), and which are obtained from a bacterium, yeast or non-*Stachybotrys* fungus, especially *C. pallescens*, *Bipolaris spicifera* (see AAY95538) and *Amerosporium atrum* (see AAY95540). The phenol oxidising enzyme is capable of modifying the colour associated with dyes or coloured compounds, and can be used for pulp and paper bleaching, for bleaching the colour of stains on fabric and for anti-dye transfer in detergent and textile applications. It may also be capable of modifying the colour in the absence or presence of an enhancer. Expression vectors and host cells comprising a nucleic acid encoding a phenol oxidising enzyme, methods for producing the phenol oxidising enzyme, and methods for constructing expression hosts are provided

XX

SQ Sequence 627 AA;

Query Match

100.0%; Score 3336; DB 3; Length 627;

Best Local Similarity 100.0%; Pred. No. 5.5e-307;
Matches 627; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 MVAKYLFSAQLASIAGIYGVALSERPAKYIDETPDEEKAALAAIVEDDPADVFRILKD 60
      |||
Db      1 MVAKYLFSAQLASIAGIYGVALSERPAKYIDETPDEEKAALAAIVEDDPADVFRILKD 60

Qy     61 WQSPEYPILFREALPIPPAKEPNKMTNPVTNKEIWYYEIVIKPFNQVYPSLRPARLVGY 120
      |||
Db     61 WQSPEYPILFREALPIPPAKEPNKMTNPVTNKEIWYYEIVIKPFNQVYPSLRPARLVGY 120

Qy    121 DGISPGPTIIVPRGTEAVVRFVNQGDRESSIHLHGSPSRAPFDGWAEDLIMKGQFKDYYY 180
      |||
Db    121 DGISPGPTIIVPRGTEAVVRFVNQGDRESSIHLHGSPSRAPFDGWAEDLIMKGQFKDYYY 180

Qy    181 PNNQAARFLWYHDHAMHVTAENAYFGQAGAYLITDPAEDALGLPSGYGKYDIPLVLSSKF 240
      |||
Db    181 PNNQAARFLWYHDHAMHVTAENAYFGQAGAYLITDPAEDALGLPSGYGKYDIPLVLSSKF 240

Qy    241 YNSDGTQLQTSVGEDNSLWGDVIHVNGQPWPFFNVEPRKYRLRFLNAAVSRNFALYFVKQQ 300
      |||
Db    241 YNSDGTQLQTSVGEDNSLWGDVIHVNGQPWPFFNVEPRKYRLRFLNAAVSRNFALYFVKQQ 300

Qy    301 ATATRLPFQVIASDAGLLTHPVQTSDIYVAAAERYEIVFDFAPYAGQTIDLRNFKANGV 360
      |||
Db    301 ATATRLPFQVIASDAGLLTHPVQTSDIYVAAAERYEIVFDFAPYAGQTIDLRNFKANGV 360

Qy    361 GTDDDYANTDKVMRFHVSSQAVVDNSVVPQAQLSQIQFPADKTGIDHHFRFHRTNSEWRIN 420
      |||
Db    361 GTDDDYANTDKVMRFHVSSQAVVDNSVVPQAQLSQIQFPADKTGIDHHFRFHRTNSEWRIN 420

Qy    421 GIGFADVQNRILAKVPRGTVELWELENSSGGWSHPHIVHLVDFRVVARYGDESTRGVMPY 480
      |||
Db    421 GIGFADVQNRILAKVPRGTVELWELENSSGGWSHPHIVHLVDFRVVARYGDESTRGVMPY 480

Qy    481 ESAGLKDVVWLGRHETVLVEAHYAPWDGVYMFHCHNLIHEDQDMMAAFDVTKLQNFYGYNE 540
      |||
Db    481 ESAGLKDVVWLGRHETVLVEAHYAPWDGVYMFHCHNLIHEDQDMMAAFDVTKLQNFYGYNE 540

Qy    541 TTDFHDPEDSRWSARPFTAADLTARSGIFSEASIRARVNELALEQPYSELAQVTASLEQY 600
      |||
Db    541 TTDFHDPEDSRWSARPFTAADLTARSGIFSEASIRARVNELALEQPYSELAQVTASLEQY 600

Qy    601 YKTNKKRQAECEDMPAGPIPRYRRFQV 627
      |||
Db    601 YKTNKKRQAECEDMPAGPIPRYRRFQV 627
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AAO18212

Query Match 100.0%; Score 3336; DB 5; Length 627;
Best Local Similarity 100.0%; Pred. No. 5.5e-307;
Matches 627; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

[illegible]

Db	61	WQSPEYPILFREALPIPPAKEPNKMTNPVTNKEIWYYEIVIKPFNQVYPSLRPARLVGY	120
Qy	121	DGISPGPTIIVPRGTEAVVRFVNQGDRESSIHLHGSPSRAPFDGWAEDLIMKGQFKDYYY	180
Db	121	DGISPGPTIIVPRGTEAVVRFVNQGDRESSIHLHGSPSRAPFDGWAEDLIMKGQFKDYYY	180
Qy	181	PNNQAARFLWYHDHAMHVTAENAYFGQAGAYLITDPAEDALGLPSGYGKYDIPLVLSSKF	240
Db	181	PNNQAARFLWYHDHAMHVTAENAYFGQAGAYLITDPAEDALGLPSGYGKYDIPLVLSSKF	240
Qy	241	YNSDGTQLQTSVGEDNSLWGDVIVHNGQPWPFFNVEPRKYRLRFLNAAVSRNFALYFVKQQ	300
Db	241	YNSDGTQLQTSVGEDNSLWGDVIVHNGQPWPFFNVEPRKYRLRFLNAAVSRNFALYFVKQQ	300
Qy	301	ATATRLPFQVIASDAGLLTHPVQTSDIYVAAAERYEIVFDFAPYAGQTIDLRNFAKANGV	360
Db	301	ATATRLPFQVIASDAGLLTHPVQTSDIYVAAAERYEIVFDFAPYAGQTIDLRNFAKANGV	360
Qy	361	GTDDDYANTDKVMRFHVSSQAVVDNSVVPAQLSQIQFPADKTGIDHHFRFHRTNSEWRIN	420
Db	361	GTDDDYANTDKVMRFHVSSQAVVDNSVVPAQLSQIQFPADKTGIDHHFRFHRTNSEWRIN	420
Qy	421	GIGFADVQNRILAKVPRGTVELWELENSSGGWSHPIHVHLVDFRVVARYGDESTRGVMPY	480
Db	421	GIGFADVQNRILAKVPRGTVELWELENSSGGWSHPIHVHLVDFRVVARYGDESTRGVMPY	480
Qy	481	ESAGLKDVVWLGRHETVLVEAHYAPWDGVYMFHCHNLIHEDQDMMAAFDVTKLQNFYNE	540
Db	481	ESAGLKDVVWLGRHETVLVEAHYAPWDGVYMFHCHNLIHEDQDMMAAFDVTKLQNFYNE	540
Qy	541	TTDFHDPEDSRWSARPFTAADLTARSGIFSEASIRARVNELALEQPYSELAQVTASLEQY	600
Db	541	TTDFHDPEDSRWSARPFTAADLTARSGIFSEASIRARVNELALEQPYSELAQVTASLEQY	600
Qy	601	YKTNKKRQAECEDMPAGPIPRYRRFQV	627
Db	601	YKTNKKRQAECEDMPAGPIPRYRRFQV	627

AA96762

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PR

PA

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DR

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1

Matches 582; Conservative 25; Mismatches 20; Indels 0; Gaps 0;

Db 1 MVAKYLF~~S~~ALOLVSI~~A~~KGIYGV~~A~~LSERPAKFVDNTPDEEKAALASIVEDDPADV~~V~~NMLKD 60

QY	61	WQSPEYPILFREALPIPPAKEPNKMTNPVTNKEIWIYYEIVIKPFNQQVYPSLRPARLVGY	120
Db	61	WQSPEYPLIFRQPLPIPPAKEPNKLTNPVTNKEIWIYYEIVIKPFNQQVYPSLRPARLVGY	120
QY	121	DGISPGPTIIVPRGTEAVVRFVNQGDRESSIHLHGSPSRAPFDGWAEDLIMKGQFKDYYY	180
Db	121	DGISPGPTIIVPRGTEAVVRFINQGDRESSIHLHGSPSRAPFDGWADDMIMKGEYKDYYY	180
QY	181	PNNQAARFLWYHDHAMHVTAENAYFGQAGAYLITDPAEDALGLPSGYGKYDIPLVLSSKF	240
Db	181	PNNQAARFLWYHDHAMHVTAENAYFGQAGAYLITDPAEDALGLPSGYGKYDIPLVLSSKY	240
QY	241	YNSDGTQLQTSVGEDNSLWGDVIHVNGQPWPFFNVEPRKYRLRFLNAAVSRNFALYFVKQQ	300
Db	241	YNADGTLKTSVGEDKSVWGDIIHVNGQPWPFFLNVEPRKYRLRFLNAAVSRNFALYFVKQD	300
QY	301	ATATRLPFQVIASDAGLLTHPVQTSDIYVAAAERYEIVFDFAPYAGQTIDLRNFAKANGV	360
Db	301	NTATRLPFQVIASDAGLLTHPVQTSDMYVAAAERYEIVFDFAPYAGQTLDLRNFAKANGI	360
QY	361	GTDDDDYANTDKVMRFHVSSQAVVDNSVVPQALSQIQFPADKTGIDHHRFRHRTNSEWRIN	420
Db	361	GTDDDDYANTDKVMRFHVSSQTVVDNSVVPQELSQIQFPADKTDIDHHRFRHRTNGEWRIN	420
QY	421	GIGFADVQNRILAKVPRGTVELWELENSSSGGWSHPIHVHLVDFRVVARYGDESTRGVMPY	480
Db	421	GIGFADVNRVLAKVPRGTVELWELENSSSGGWSHPIHVHLVDFRVVARYGDEGTRGVMPY	480
QY	481	ESAGLKDVVWLGRHETVLVEAHYAPWDGVYMFHCHNLIHEDQDMMAAFDVTKLQNFYNE	540
Db	481	EAAGLKDVVWLGRHETVLVEAHYAPWDGVYMFHCHNLIHEDQDMMAAFDVTKLQNFYNE	540
QY	541	TTDFHDPEDSRWSARPFTAADLTARSGIFSEASIRARVNELALEQPYSELAQVTASLEQY	600
Db	541	TTDFHDPEDPRWSARPFTAGDLTARSGIFSEESIRARVNELALEQPYSELAQVTASLEQY	600
QY	601	YKTNKKRQAECEDMPAGPIPRYRRFQV	627
Db	601	YKTNQKRHDECEDMPAGPIPRYRRFQV	627

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- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
- 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
- 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
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- 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		%					
No.	Score	Query	Match	Length	ID	Description	
1	3336	100.0	627	13	US-10-080-210-7	Sequence 7, Appli	
2	3168	95.0	627	9	US-09-338-723A-4	Sequence 4, Appli	
3	3168	95.0	627	13	US-10-080-210-4	Sequence 4, Appli	
4	1929.5	57.8	594	9	US-09-338-723A-2	Sequence 2, Appli	
5	1929.5	57.8	594	13	US-10-080-210-2	Sequence 2, Appli	
6	1929.5	57.8	594	13	US-10-080-233-2	Sequence 2, Appli	
7	1795	53.8	572	9	US-09-942-185-4	Sequence 4, Appli	
8	1795	53.8	572	14	US-10-241-602-4	Sequence 4, Appli	

Database : PIR_78:*
 1: pir1:*
 2: pir2:*
 3: pir3:*
 4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	% Query		Match	Length	DB	ID	Description
	Score	Match					
1	1795	53.8	572	2	B48521	bilirubin oxidase	
2	689	20.7	513	2	F69604	spore coat protein	
3	457.5	13.7	568	2	B86364	hypothetical prote	
4	432.5	13.0	591	2	G96734	spore coat protein	
5	427.5	12.8	527	2	C70397	periplasmic cell d	
6	426.5	12.8	533	2	AC0414	probable exported	
7	423	12.7	494	2	AC3582	probable blue-copp	
8	412	12.4	516	2	C64735	probable copper-bi	
9	409	12.3	516	2	G90644	hypothetical prote	
10	409	12.3	516	2	G85495	hypothetical prote	
11	390	11.7	536	2	AF0523	probable multicopp	
12	320.5	9.6	470	2	E91116	suppressor of ftsI	
13	320.5	9.6	470	2	E85961	suppressor of ftsI	
14	319.5	9.6	470	2	G65088	sufI protein precu	
15	310.5	9.3	470	2	AD0888	SufI protein [impo	
16	296.5	8.9	513	2	G81298	probable periplasm	
17	291	8.7	474	2	AD0083	probable cell divi	
18	267	8.0	463	2	G83175	probable metallo-o	
19	263	7.9	1662	2	T18540	mofA protein precu	
20	250	7.5	721	2	H82528	L-ascorbate oxidas	
21	233.5	7.0	311	2	H64157	sufI protein homol	
22	225.5	6.8	500	2	B83910	hypothetical prote	
23	217	6.5	520	2	JC5356	laccase (EC 1.10.3	

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	1795	53.8	572	1	BLRO_MYRVE	Q12737 myrothecium
2	689	20.7	513	1	COTA_BACSU	P07788 bacillus su
3	528.5	15.8	642	1	PHSA_STRAT	Q53692 streptomyce
4	426.5	12.8	533	1	CUEO_YERPE	Q8zbk0 yersinia pe
5	412	12.4	516	1	CUEO_ECOLI	P36649 escherichia
6	409	12.3	516	1	CUEO_ECO57	Q8x947 escherichia
7	390	11.7	536	1	CUEO_SALTI	Q8z9e1 salmonella
8	390	11.7	536	1	CUEO_SALTY	Q8zrs2 salmonella
9	319.5	9.6	470	1	SUFI_ECOLI	P26648 escherichia
10	310.5	9.3	470	1	SUFI_SALTY	P40799 salmonella
11	233.5	7.0	311	1	SUFI_HAEIN	P44847 haemophilus
12	217	6.5	520	1	LAC4_TRAVI	Q99055 trametes vi
13	216	6.5	520	1	LAC4_TRAVE	Q12719 trametes ve
14	210.5	6.3	591	1	LAC1_CRYPA	Q03966 cryphonectr
15	210	6.3	619	1	LAC1_NEUCR	P06811 neurospora
16	200	6.0	619	1	LAC2_NEUCR	P10574 neurospora
17	197	5.9	529	1	LAC1_PLEOS	Q12729 pleurotus o
18	195.5	5.9	533	1	LAC2_PLEOS	Q12739 pleurotus o
19	194	5.8	589	1	CPA2_PSESM	P59571 pseudomonas

Database : SPTREMBL_25:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvirus:*
- 16: sp_bacteriap:*
- 17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	1761.5	52.8	602	3	Q9P8C3	Q9p8c3 acremonium
2	624.5	18.7	475	2	Q93M03	Q93m03 streptomyce
3	611	18.3	513	16	Q8CXJ7	Q8cxj7 oceanobacil
4	534	16.0	431	2	Q8RMC6	Q8rmc6 streptomyce
5	513.5	15.4	631	2	Q8GB87	Q8gb87 streptomyce
6	508	15.2	583	16	Q8FQU9	Q8fqu9 corynebacte
7	487	14.6	511	16	Q8NRU6	Q8nru6 corynebacte
8	483.5	14.5	582	10	Q9AWU4	Q9awu4 oryza sativ
9	467.5	14.0	637	10	Q9FTS3	Q9fts3 oryza sativ
10	467	14.0	501	16	Q88ZG5	Q88zg5 lactobacill

RESULT 2

AR275740

LOCUS AR275740 858 bp DNA linear PAT 10-APR-2003

DEFINITION Sequence 8 from patent US 6509307.

ACCESSION AR275740

VERSION AR275740.1 GI:29709289

KEYWORDS .

SOURCE Unknown.

ORGANISM Unknown.

Unclassified.

REFERENCE 1 (bases 1 to 858)

AUTHORS Bodie,E.A., van der Velden,S., de Vries,C.H. and Wang,H.

TITLE Detergent compositions comprising phenol oxidizing enzymes from fungi

JOURNAL Patent: US 6509307-A 8 21-JAN-2003;

FEATURES Location/Qualifiers

source 1. .858

/organism="unknown"

/mol_type="genomic DNA"

ORIGIN

Query Match 99.0%; Score 849; DB 6; Length 858;

Best Local Similarity 100.0%; Pred. No. 5.6e-206;

Matches 858; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 CACCGCCGAGAACGCTTACTTTGGTCAAGCTGGCTTTTACATTCTGCACGACCCCGCTGA 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 CACCGCCGAGAACGCTTACTTTGGTCAAGCTGGCTTTTACATTCTGCACGACCCCGCTGA 60

Qy     61 AGATGCATTGGGTCTGCCTTCTGGCAAGTATGATGTACCTCTTGCACTGTCCTCCAAGCA 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 AGATGCATTGGGTCTGCCTTCTGGCAAGTATGATGTACCTCTTGCACTGTCCTCCAAGCA 120

Qy    121 GTACAACAGCGACGGTACCCTCTTCGACCCCAAGGACGAGACCGATTCACTGTTTCGGCGA 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 GTACAACAGCGACGGTACCCTCTTCGACCCCAAGGACGAGACCGATTCACTGTTTCGGCGA 180

Qy    181 TGTCATCCACGTCAACGGACAGCCATGGCCCTACTTTAAGGTCGAGCCTCGCAAGTACCG 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 TGTCATCCACGTCAACGGACAGCCATGGCCCTACTTTAAGGTCGAGCCTCGCAAGTACCG 240

Qy    241 TCTCCGCTTCCTCAATGCTGCTATCAGCCGTGCCTTCAAGCTCACTTTTCGAGGCTGATGG 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 TCTCCGCTTCCTCAATGCTGCTATCAGCCGTGCCTTCAAGCTCACTTTTCGAGGCTGATGG 300

Qy    301 CAAAGTGATCAACTTTCCTGTGCATCGGTGCCGATACTGGTCTCTTGACCAAGCCTGTTCA 360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 CAAAGTGATCAACTTTCCTGTGCATCGGTGCCGATACTGGTCTCTTGACCAAGCCTGTTCA 360

Qy    361 GACAAGCAACCTTGAGATCTCTATGGCCGAGCGCTGGGAGGTTGTTTTTGACTTCAGCCA 420
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 GACAAGCAACCTTGAGATCTCTATGGCCGAGCGCTGGGAGGTTGTTTTTGACTTCAGCCA 420

Qy    421 ATTTTCCGGGAAGAACGTCAACCTCAAGAACGGTCGCGATGTGCAGCACGATGAGGACTA 480
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 ATTTTCCGGGAAGAACGTCAACCTCAAGAACGGTCGCGATGTGCAGCACGATGAGGACTA 480

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Qy	481	CAACTCCACCGACAAAGTCATGCAGTTCGTTGTTGGCAAGGATGTTACGAGCCAGGCTGG	540
Db	481	CAACTCCACCGACAAAGTCATGCAGTTCGTTGTTGGCAAGGATGTTACGAGCCAGGCTGG	540
Qy	541	TAATGGCAACCTTCCCGGCTCTCTGCGCACTGTTCCCTTCCCTCCTAAGAAGGGGCGGAG	600
Db	541	TAATGGCAACCTTCCCGGCTCTCTGCGCACTGTTCCCTTCCCTCCTAAGAAGGGGCGGAG	600
Qy	601	TCGACAGGAGCTTCAAGTTCGGCAGGGACCGGTGGCCAGTGGACTGTTAATGGCTTGACC	660
Db	601	TCGACAGGAGCTTCAAGTTCGGCAGGGACCGGTGGCCAGTGGACTGTTAATGGCTTGACC	660
Qy	661	TTCGCTGATGTCAACAACCGCATCCTGGCTAAGCCCCAACGTGGTGCCATCGAGGTTTT	720
Db	661	TTCGCTGATGTCAACAACCGCATCCTGGCTAAGCCCCAACGTGGTGCCATCGAGGTTTT	720
Qy	721	GGGAGCTTTGAGAACTTCCAGCGGNGGNTGGTCTTACCCTTGTCACATCCACCTGGGTC	780
Db	721	GGGAGCTTTGAGAACTTCCAGCGGNGGNTGGTCTTACCCTTGTCACATCCACCTGGGTC	780
Qy	781	GACTTTCCAGATNCTTGTCTTGCACTGGANGCAAGGCNCCCCGTTNTAACTNCNANAAAG	840
Db	781	GACTTTCCAGATNCTTGTCTTGCACTGGANGCAAGGCNCCCCGTTNTAACTNCNANAAAG	840
Qy	841	GAAGCACTTTCAAGGGCG	858
Db	841	GAAGCACTTTCAAGGGCG	858

Result		%					
No.	Score	Query	Match	Length	DB	ID	Description
1	3336	100.0	627	26	US-10-080-210-7		Sequence 7, Appli
2	3168	95.0	627	17	US-09-338-723-4		Sequence 4, Appli
3	3168	95.0	627	17	US-09-338-723A-4		Sequence 4, Appli
4	3168	95.0	627	26	US-10-080-210-4		Sequence 4, Appli
5	1929.5	57.8	594	16	US-09-218-702-2		Sequence 2, Appli
6	1929.5	57.8	594	16	US-09-273-957-2		Sequence 2, Appli
7	1929.5	57.8	594	17	US-09-338-723-2		Sequence 2, Appli
8	1929.5	57.8	594	17	US-09-338-723A-2		Sequence 2, Appli